



#7

SEQUENCE LISTING

5 <110> Schweifer, Norbert
 Scherl-Mostageer, Marwa
 Sommergruber, Wolfgang
 Abseher, Roger

<120> Tumour-associated Antigen (B345)

10 <130> 0652.2280001/EKS/AES

<140>
 <141>

15 <150> DE 100 33 080.0
 <151> 2000-07-07

<150> DE 101 19 294.0
 <151> 2001-04-19

20 <150> US 60/243,158
 <151> 2000-10-25

25 <150> US 60/297,747
 <151> 2001-06-14

<160> 40

30 <170> PatentIn Ver. 2.1

<210> 1
 <211> 5897
 35 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 40 <222> (1)..(214)

<220>
 <221> CDS
 <222> (215)..(2464)

45 <220>
 <221> 3'UTR
 <222> (2465)..(5897)

50 <400> 1
 cttgagatat tagaattcgc gactcctgaa ctgcgggggc tctatcgac tgctaggggt
 60

55 tctgctgctg ggtgcggcgc gcctgccgcg cggggcagaa gcttttgaga ttgctctgcc
 120

acgagaaagc aacattacag ttctcataaa gctggggacc ccgactctgc tggcaaaacc
 180

ctgttacatc gtcatttcta aaagacatat aacc atg ttg tcc atc aag tct gga
 235

5 Met Leu Ser Ile Lys Ser Gly
 1 5

gaa aga ata gtc ttt acc ttt agc tgc cag agt cct gag aat cac ttt
 283

10 Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser Pro Glu Asn His Phe
 10 15 20

gtc ata gag atc cag aaa aat att gac tgt atg tca ggc cca tgt cct
 331

15 Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met Ser Gly Pro Cys Pro
 25 30 35

ttt ggg gag gtt cag ctt cag ccc tcg aca tcg ttg ttg cct acc ctc
 379

20 Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser Leu Leu Pro Thr Leu
 40 45 50 55

aac aga act ttc atc tgg gat gtc aaa gct cat aag agc atc ggt tta
 427

25 Asn Arg Thr Phe Ile Trp Asp Val Lys Ala His Lys Ser Ile Gly Leu
 60 65 70

gag ctg cag ttt tcc atc cct cgc ctg agg cag atc ggt ccg ggt gag
 475

30 Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln Ile Gly Pro Gly Glu
 75 80 85

agc tgc cca gac gga gtc act cac tcc atc agc ggc cga atc gat gcc
 523

35 Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser Gly Arg Ile Asp Ala
 90 95 100

acc gtg gtc agg atc gga acc ttc tgc agc aat ggc act gtg tcc cgg
 571

40 Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn Gly Thr Val Ser Arg
 105 110 115

atc aag atg caa gaa gga gtg aaa atg gcc tta cac ctc cca tgg ttc
 619

45 Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu His Leu Pro Trp Phe
 120 125 130 135

cac ccc aga aat gtc tcc ggc ttc agc att gca aac cgc tca tct ata
 667

50 His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala Asn Arg Ser Ser Ile
 140 145 150

aaa cgt ctg tgc atc atc gag tct gtg ttt gag ggt gaa ggc tca gca
 715

55 Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu Gly Glu Gly Ser Ala
 155 160 165

acc ctg atg tct gcc aac tac cca gaa ggc ttc cct gag gat gag ctg
 763
 Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe Pro Glu Asp Glu Leu
 170 175 180
 5
 atg acg tgg cag ttt gtc gtt cct gca cac ctg cgg gcc agc gtc tcc
 811
 Met Thr Trp Gln Phe Val Val Pro Ala His Leu Arg Ala Ser Val Ser
 185 190 195
 10
 ttc ctc aac ttc aac ctc tcc aac tgt gag agg aag gag gag cgg gtt
 859
 Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg Lys Glu Glu Arg Val
 200 205 210 215
 15
 gaa tac tac atc ccg ggc tcc acc acc aac ccc gag gtg ttc aag ctg
 907
 Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro Glu Val Phe Lys Leu
 220 225 230
 20
 gag gac aag cag cct ggg aac atg gcg ggg aac ttc aac ctc tct ctg
 955
 Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn Phe Asn Leu Ser Leu
 235 240 245
 25
 caa ggc tgt gac caa gat gcc caa agt cca ggg atc ctc cgg ctg cag
 1003
 Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly Ile Leu Arg Leu Gln
 250 255 260
 30
 ttc caa gtt ttg gtc caa cat cca caa aat gaa agc aat aaa atc tac
 1051
 Phe Gln Val Leu Val Gln His Pro Gln Asn Glu Ser Asn Lys Ile Tyr
 265 270 275
 35
 gtg gtt gac ttg agt aat gag cga gcc atg tca ctc acc atc gag cca
 1099
 40 Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser Leu Thr Ile Glu Pro
 280 285 290 295
 cgg ccc gtc aaa cag agc cgc aag ttt gtc cct ggc tgt ttc gtg tgt
 1147
 45 Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro Gly Cys Phe Val Cys
 300 305 310
 cta gaa tct cgg acc tgc agt agc aac ctc acc ctg aca tct ggc tcc
 1195
 50 Leu Glu Ser Arg Thr Cys Ser Ser Asn Leu Thr Leu Thr Ser Gly Ser
 315 320 325
 aaa cac aaa atc tcc ttc ctt tgt gat gat ctg aca cgt ctg tgg atg
 1243
 55 Lys His Lys Ile Ser Phe Leu Cys Asp Asp Leu Thr Arg Leu Trp Met
 330 335 340

aat gtg gaa aaa acc ata agc tgc aca gac cac cgg tac tgc caa agg
 1291
 Asn Val Glu Lys Thr Ile Ser Cys Thr Asp His Arg Tyr Cys Gln Arg
 345 350 355
 5
 aaa tcc tac tca ctc cag gtg ccc agt gac atc ctc cac ctg cct gtg
 1339
 Lys Ser Tyr Ser Leu Gln Val Pro Ser Asp Ile Leu His Leu Pro Val
 360 365 370 375
 10
 gag ctg cat gac ttc tcc tgg aag ctg ctg gtg ccc aag gac agg ctc
 1387
 Glu Leu His Asp Phe Ser Trp Lys Leu Leu Val Pro Lys Asp Arg Leu
 380 385 390
 15
 agc ctg gtg ctg gtg cca gcc cag aag ctg cag cag cat aca cac gag
 1435
 Ser Leu Val Leu Val Pro Ala Gln Lys Leu Gln Gln His Thr His Glu
 395 400 405
 20
 aag ccc tgc aac acc agc ttc agc tac ctc gtg gcc agt gcc ata ccc
 1483
 Lys Pro Cys Asn Thr Ser Phe Ser Tyr Leu Val Ala Ser Ala Ile Pro
 410 415 420
 25
 agc cag gac ctg tac ttc ggc tcc ttc tgc ccg gga ggc tct atc aag
 1531
 Ser Gln Asp Leu Tyr Phe Gly Ser Phe Cys Pro Gly Gly Ser Ile Lys
 425 430 435
 30
 cag atc cag gtg aag cag aac atc tcg gtg acc ctt cgc acc ttt gcc
 1579
 Gln Ile Gln Val Lys Gln Asn Ile Ser Val Thr Leu Arg Thr Phe Ala
 440 445 450 455
 35
 ccc agc ttc caa caa gag gcc tcc agg cag ggt ctg acg gtg tcc ttt
 1627
 Pro Ser Phe Gln Gln Glu Ala Ser Arg Gln Gly Leu Thr Val Ser Phe
 460 465 470
 40
 ata cct tat ttc aaa gag gaa ggc gtt ttc acg gtg acc cct gac aca
 1675
 Ile Pro Tyr Phe Lys Glu Glu Gly Val Phe Thr Val Thr Pro Asp Thr
 475 480 485
 45
 aaa agc aag gtc tac ctg agg acc ccc aac tgg gac cgg ggc ctg cca
 1723
 Lys Ser Lys Val Tyr Leu Arg Thr Pro Asn Trp Asp Arg Gly Leu Pro
 490 495 500
 50
 tcc ctc acc tct gtg tcc tgg aac atc agc gtg ccc aga gac cag gtg
 1771
 Ser Leu Thr Ser Val Ser Trp Asn Ile Ser Val Pro Arg Asp Gln Val
 505 510 515
 55
 gcc tgc ctg act ttc ttt aag gag cgg agc ggc gtg gtc tgc cag aca
 1819

	Ala	Cys	Leu	Thr	Phe	Phe	Lys	Glu	Arg	Ser	Gly	Val	Val	Cys	Gln	Thr	
	520					525					530					535	
5	ggg	cgc	gca	ttc	atg	atc	atc	cag	gag	cag	cgg	acc	cgg	gct	gag	gag	
	1867																
	Gly	Arg	Ala	Phe	Met	Ile	Ile	Gln	Glu	Gln	Arg	Thr	Arg	Ala	Glu	Glu	
					540					545					550		
10	atc	ttc	agc	ctg	gac	gag	gat	gtg	ctc	ccc	aag	cca	agc	ttc	cac	cat	
	1915																
	Ile	Phe	Ser	Leu	Asp	Glu	Asp	Val	Leu	Pro	Lys	Pro	Ser	Phe	His	His	
				555					560					565			
15	cac	agc	ttc	tgg	gtc	aac	atc	tct	aac	tgc	agc	ccc	acg	agc	ggc	aag	
	1963																
	His	Ser	Phe	Trp	Val	Asn	Ile	Ser	Asn	Cys	Ser	Pro	Thr	Ser	Gly	Lys	
			570					575					580				
20	cag	cta	gac	ctg	ctc	ttc	tcg	gtg	aca	ctt	acc	cca	agg	act	gtg	gac	
	2011																
	Gln	Leu	Asp	Leu	Leu	Phe	Ser	Val	Thr	Leu	Thr	Pro	Arg	Thr	Val	Asp	
		585					590					595					
25	ttg	act	gtc	atc	ctc	atc	gca	gcg	gtg	gga	ggt	gga	gtc	tta	ctg	ctg	
	2059																
	Leu	Thr	Val	Ile	Leu	Ile	Ala	Ala	Val	Gly	Gly	Gly	Val	Leu	Leu	Leu	
	600					605					610					615	
30	tct	gcc	ctc	ggg	ctc	atc	att	tgc	tgt	gtg	aaa	aag	aag	aaa	aag	aag	
	2107																
	Ser	Ala	Leu	Gly	Leu	Ile	Ile	Cys	Cys	Val	Lys	Lys	Lys	Lys	Lys	Lys	
					620					625						630	
35	aca	aac	aag	ggc	ccc	gct	gtg	ggt	atc	tac	aat	ggc	aac	atc	aat	act	
	2155																
	Thr	Asn	Lys	Gly	Pro	Ala	Val	Gly	Ile	Tyr	Asn	Gly	Asn	Ile	Asn	Thr	
				635					640					645			
40	gag	atg	cca	ggc	agc	caa	aaa	agt	ttc	aga	aag	ggc	gaa	agg	aca	atg	
	2203																
	Glu	Met	Pro	Gly	Ser	Gln	Lys	Ser	Phe	Arg	Lys	Gly	Glu	Arg	Thr	Met	
			650					655					660				
45	act	ccc	atg	tgt	atg	cag	tca	tcg	agg	aca	cca	tgg	tat	atg	ggc	atc	
	2251																
	Thr	Pro	Met	Cys	Met	Gln	Ser	Ser	Arg	Thr	Pro	Trp	Tyr	Met	Gly	Ile	
		665					670					675					
50	tgc	tac	agg	att	cca	gcg	gct	cct	tcc	tgc	agc	cag	agg	tgg	aca	cct	
	2299																
	Cys	Tyr	Arg	Ile	Pro	Ala	Ala	Pro	Ser	Cys	Ser	Gln	Arg	Trp	Thr	Pro	
	680					685					690					695	
55	acc	ggc	cgt	tcc	agg	gca	cca	tgg	ggg	tct	gtc	ctc	cct	ccc	cac	cca	
	2347																
	Thr	Gly	Arg	Ser	Arg	Ala	Pro	Trp	Gly	Ser	Val	Leu	Pro	Pro	His	Pro	
					700					705					710		

cca tat gct cca ggg ccc caa ctg caa agt tgg cca ctg agg agc cac
 2395
 Pro Tyr Ala Pro Gly Pro Gln Leu Gln Ser Trp Pro Leu Arg Ser His
 715 720 725

5

ctc ctc gct ccc ctc ctg agt ctg aga gtg aac cgt aca cct tct ccc
 2443
 10 Leu Leu Ala Pro Leu Leu Ser Leu Arg Val Asn Arg Thr Pro Ser Pro
 730 735 740

atc cca aca atg ggg atg taa gcagcaagga cacagacatt cccttactga
 2494
 15 Ile Pro Thr Met Gly Met
 745 750

acactcagga gcccatggag ccagcagaat aacttgatcc attccagacg ctttgctgag
 2554
 20 tttcataaag cagggcactg agacaccggt ccgtgttcct aaccagaaat cctaaagaag
 2614

aggaattata cagaaggaac agcaggaggt tttcctggac accgccaact tcacattgct
 2674
 25 cagtggactc attctaaggg caagacattg aaaatgatga attccaatct ggatacagtc
 2734

atgacagctc atgtgctcct caacttaggc tgtgcgggta gccagcctgt aatgagagga
 2794
 30 gagaggcctg agtcacctag cataggggtg cagcaagccc tggattcaga gtgttaaaca
 2854

35 gaggcttgcc ctcttcagga caacagttcc aattccaagg agcctacctg aggtccctac
 2914

tctcactggg gtcccagga tgaaaacgac aatgtgcctt tttattatta tttatttggt
 2974
 40 ggtcctgtgt tatttaagag atcaaatgta taaccaccta gctcttttca cctgacttag
 3034

taataactca tactaactgg tttggatgcc tgggttgtga cttctactga ccgctagata
 3094
 45 aacgtgtgcc tgtccccag gtggtgggaa taatttaca tctgtccaac cagaaaagaa
 3154

50 tgtgtgtggt tgagcagcat tgacacatat ctgctttgat aagagacttc ctgattctct
 3214

aggtcgggtc gtggttatcc cattgtggaa attcatcttg aatccattg tcctatagtc
 3274
 55 ctagcaataa gagaaatttc ctcaagtttc catgtgcggt tctcctagct gcagcaatac
 3334

tttgacattt aaagagaaat ttagagaata ttctcatcct ctaaaaatgt ttaaatatat
 3394

5 accaaacagt ggccccctgc attagttttc tgttgccact gcaaccatt acttggtage
 3454

ttaaaaacaa cacattagct tatagtcctg gggatcagaa ttccaaaatg gatgtccctg
 3514

10 aatgaaaatc aaggtgtcag cagagctgtg ctcttctga aggtctagg gagaagccgg
 3574

15 ttcttgcca tttcaagctt ctagaggctg gctgcattcc caggctccag tggctggtca
 3634

agcttttctc acatggcatc actgtgacac tggccctccc acttccctct ttgacttaca
 3694

20 aagcccacca ggaagatcca ggataatctc tccatctaaa gatccttcat catcctggaa
 3754

gagccttttg ccatgcaaga caacatagcc acagggtgggg attaggacca ggacatcttt
 3814

25 ggggtgctgt tattctgcct accacacctt cctgccacbg actcccacag gagaggctac
 3874

30 aaaatgatct ggcgcacagg gatgttttgt ttagcttgcg gactctaaca cttaaaaaaa
 3934

cccagatca gaagatctgg ccatgctggg gctcacattc tcacctagca acaactggct
 3994

35 ggagctgggc accagctctg cctttagaag ggggtgtccac ttcaccaggt caccacagcc
 4054

cactacgc cctatcactt cccacaatga ggctaagtgt ttgtttctac tgatcaatgc
 4114

40 ccctgcaggt tgcatttatt gtaatgaaaa agaaagactg ggattaatct ctaatcaggt
 4174

45 gagtagacca tgagaccaat gtgtgctcac attacccttt ttcttttttt tctttttctt
 4234

tttctttttt tttttaatgt gagacaggat ctcatctgt tgcctaggct ggagtgcagt
 4294

50 ggcgcaatct cggctcactg caacctctgc ctctgggct caagcaattc tcccacctca
 4354

gcctcccaa tagctgggat cactggcaca aaccaccatg cccagctaatt tttgtatttt
 4414

55 ttgtagagac agggtttcac catgttgccc aggtggtct caacctctg ggctcaagca
 4474

atcctcctgc ctcggcctcc caaagtgctg ggattacaga tgtgagccac cgcattccagc
 4534

5 cccacaccct catttatacc aattacctgc ccagtaactg tggacttttg cttcctcacc
 4594

cctgctctga tctggaagga gagggattat gttatagctt gtcagcacag tcccaagttc
 4654

10 aatattttctg cggcaaaaac ttccttcaaa aaataaatgt acttcattgt attcaatgaa
 4714

ttcaccttgg aaatgcaccg cctcaacttg ttcacatggc ataaatgaaa ggaattttat
 4774

15 agtctcctaa atggcgtgta ctgcaagacc tcttgaacac tttccagagg ataggatatt
 4834

20 taagtcatgc ccttggcggt gcctatggca cctttccctt ctgaaagtct ggttcttgcc
 4894

cagtgaacct tggccttggt agccgagatg ctgacctgc ataaagggcc aaaggagggc
 4954

25 tgccggttcc ttccctcact gaagagccct tatttgaatt cactgtgtgg agccctagcc
 5014

ctccattctc gacattcccc aacctcccag ccccttccaa gcaggactag gtgccttgca
 5074

30 ttccacccaa ggtgggattg gccttcttta ggctggctac ttgtcaccat caccgacatc
 5134

actggtgcct gcaaggacac cacgtggcca ttttcttca actgagggct caaaactcct
 5194

ggacaagttg ctggctcctg agaccagtat ttctggagm tgtgcctcag tgaagggggc
 5254

40 cagcctgagg aaccctggct cttttcttta aagcccaggc cccacttaca taaaacattt
 5314

cagggtcact ggaaacagtg aagtgccatt tgtngaagcc tactgnatgc cagcccactg
 5374

45 ctcatccacg tggatgcca tgcctacgag gaaggccagc gcatgcagga ntggtctcta
 5434

atgntgtggt cattgcacag aagggaagg tctcaaggaa gagtcaactg ggacaagcac
 5494

aagcccaccg gacatggcct tggtaaaggt tagcagactg gtgtgtgtgg atctgcagtg
 5554

55 cttcactgga aataatttat tcattgcaga tacttttttag gtggcatttt attcatttcc
 5614

tgtgcttttaa ataaacaaat gtaccaaaaa acaagtatca agctgttttaa gtgcttcggc
 5674
 5 tacttggtccc ctggttcagt agaggccccg gtttcccagt tggtgactgt gacaggctca
 5734
 gcatgggctc agcagatgct gtcttaattt gtggatgata cagaaagcca ggctttggga
 5794
 10 tacaagttct ttcctcttca tttgatgccg tgcactgtgt gaagcagatg tttttgtccg
 5854
 gaaataaaaa taatagtctt ggagtctcgc caaaaaaaaaa aag
 5897
 15
 <210> 2
 <211> 749
 20 <212> PRT
 <213> Homo sapiens
 <400> 2
 25 Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys
 1 5 10 15
 Gln Ser Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn Ile Asp
 20 25 30
 30 Cys Met Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln Pro Ser
 35 40 45
 Thr Ser Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp Val Lys
 50 55 60
 35 Ala His Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro Arg Leu
 65 70 75 80
 Arg Gln Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr His Ser
 40 85 90 95
 Ile Ser Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr Phe Cys
 100 105 110
 45 Ser Asn Gly Thr Val Ser Arg Ile Lys Met Gln Glu Gly Val Lys Met
 115 120 125
 Ala Leu His Leu Pro Trp Phe His Pro Arg Asn Val Ser Gly Phe Ser
 130 135 140
 50 Ile Ala Asn Arg Ser Ser Ile Lys Arg Leu Cys Ile Ile Glu Ser Val
 145 150 155 160
 Phe Glu Gly Glu Gly Ser Ala Thr Leu Met Ser Ala Asn Tyr Pro Glu
 55 165 170 175
 Gly Phe Pro Glu Asp Glu Leu Met Thr Trp Gln Phe Val Val Pro Ala
 180 185 190

	His	Leu	Arg	Ala	Ser	Val	Ser	Phe	Leu	Asn	Phe	Asn	Leu	Ser	Asn	Cys
			195					200					205			
5	Glu	Arg	Lys	Glu	Glu	Arg	Val	Glu	Tyr	Tyr	Ile	Pro	Gly	Ser	Thr	Thr
		210					215					220				
	Asn	Pro	Glu	Val	Phe	Lys	Leu	Glu	Asp	Lys	Gln	Pro	Gly	Asn	Met	Ala
	225					230					235					240
10	Gly	Asn	Phe	Asn	Leu	Ser	Leu	Gln	Gly	Cys	Asp	Gln	Asp	Ala	Gln	Ser
					245					250					255	
	Pro	Gly	Ile	Leu	Arg	Leu	Gln	Phe	Gln	Val	Leu	Val	Gln	His	Pro	Gln
15				260					265					270		
	Asn	Glu	Ser	Asn	Lys	Ile	Tyr	Val	Val	Asp	Leu	Ser	Asn	Glu	Arg	Ala
			275					280					285			
20	Met	Ser	Leu	Thr	Ile	Glu	Pro	Arg	Pro	Val	Lys	Gln	Ser	Arg	Lys	Phe
		290					295					300				
	Val	Pro	Gly	Cys	Phe	Val	Cys	Leu	Glu	Ser	Arg	Thr	Cys	Ser	Ser	Asn
	305					310					315					320
25	Leu	Thr	Leu	Thr	Ser	Gly	Ser	Lys	His	Lys	Ile	Ser	Phe	Leu	Cys	Asp
					325					330					335	
	Asp	Leu	Thr	Arg	Leu	Trp	Met	Asn	Val	Glu	Lys	Thr	Ile	Ser	Cys	Thr
30				340					345					350		
	Asp	His	Arg	Tyr	Cys	Gln	Arg	Lys	Ser	Tyr	Ser	Leu	Gln	Val	Pro	Ser
			355					360					365			
35	Asp	Ile	Leu	His	Leu	Pro	Val	Glu	Leu	His	Asp	Phe	Ser	Trp	Lys	Leu
		370					375					380				
	Leu	Val	Pro	Lys	Asp	Arg	Leu	Ser	Leu	Val	Leu	Val	Pro	Ala	Gln	Lys
	385					390					395					400
40	Leu	Gln	Gln	His	Thr	His	Glu	Lys	Pro	Cys	Asn	Thr	Ser	Phe	Ser	Tyr
					405					410					415	
	Leu	Val	Ala	Ser	Ala	Ile	Pro	Ser	Gln	Asp	Leu	Tyr	Phe	Gly	Ser	Phe
45				420					425					430		
	Cys	Pro	Gly	Gly	Ser	Ile	Lys	Gln	Ile	Gln	Val	Lys	Gln	Asn	Ile	Ser
			435					440					445			
50	Val	Thr	Leu	Arg	Thr	Phe	Ala	Pro	Ser	Phe	Gln	Gln	Glu	Ala	Ser	Arg
		450					455					460				
	Gln	Gly	Leu	Thr	Val	Ser	Phe	Ile	Pro	Tyr	Phe	Lys	Glu	Glu	Gly	Val
	465					470					475					480
55	Phe	Thr	Val	Thr	Pro	Asp	Thr	Lys	Ser	Lys	Val	Tyr	Leu	Arg	Thr	Pro
					485					490					495	

	Asn	Trp	Asp	Arg	Gly	Leu	Pro	Ser	Leu	Thr	Ser	Val	Ser	Trp	Asn	Ile	
				500					505					510			
5	Ser	Val	Pro	Arg	Asp	Gln	Val	Ala	Cys	Leu	Thr	Phe	Phe	Lys	Glu	Arg	
			515					520					525				
	Ser	Gly	Val	Val	Cys	Gln	Thr	Gly	Arg	Ala	Phe	Met	Ile	Ile	Gln	Glu	
		530					535					540					
10	Gln	Arg	Thr	Arg	Ala	Glu	Glu	Ile	Phe	Ser	Leu	Asp	Glu	Asp	Val	Leu	
	545					550					555					560	
	Pro	Lys	Pro	Ser	Phe	His	His	His	Ser	Phe	Trp	Val	Asn	Ile	Ser	Asn	
					565					570					575		
15	Cys	Ser	Pro	Thr	Ser	Gly	Lys	Gln	Leu	Asp	Leu	Leu	Phe	Ser	Val	Thr	
				580					585					590			
	Leu	Thr	Pro	Arg	Thr	Val	Asp	Leu	Thr	Val	Ile	Leu	Ile	Ala	Ala	Val	
20			595					600					605				
	Gly	Gly	Gly	Val	Leu	Leu	Leu	Ser	Ala	Leu	Gly	Leu	Ile	Ile	Cys	Cys	
		610					615					620					
25	Val	Lys	Lys	Lys	Lys	Lys	Lys	Thr	Asn	Lys	Gly	Pro	Ala	Val	Gly	Ile	
	625					630					635					640	
	Tyr	Asn	Gly	Asn	Ile	Asn	Thr	Glu	Met	Pro	Gly	Ser	Gln	Lys	Ser	Phe	
					645					650					655		
30	Arg	Lys	Gly	Glu	Arg	Thr	Met	Thr	Pro	Met	Cys	Met	Gln	Ser	Ser	Arg	
				660					665					670			
	Thr	Pro	Trp	Tyr	Met	Gly	Ile	Cys	Tyr	Arg	Ile	Pro	Ala	Ala	Pro	Ser	
35			675					680					685				
	Cys	Ser	Gln	Arg	Trp	Thr	Pro	Thr	Gly	Arg	Ser	Arg	Ala	Pro	Trp	Gly	
		690					695					700					
40	Ser	Val	Leu	Pro	Pro	His	Pro	Pro	Tyr	Ala	Pro	Gly	Pro	Gln	Leu	Gln	
	705					710					715					720	
	Ser	Trp	Pro	Leu	Arg	Ser	His	Leu	Leu	Ala	Pro	Leu	Leu	Ser	Leu	Arg	
					725					730					735		
45	Val	Asn	Arg	Thr	Pro	Ser	Pro	Ile	Pro	Thr	Met	Gly	Met				
				740					745								
50																	
	<210> 3																
	<211> 6163																
	<212> DNA																
	<213> Homo sapiens																
55																	
	<220>																
	<221> 5'UTR																
	<222> (1)..(282)																

```

5    <220>
    <221> GC_signal
    <222> (147)..(157)

10   <220>
    <221> misc_feature
    <222> (201)..(209)
    <223> cap signal; Transcription start

15   <220>
    <221> 3'UTR
    <222> (2794)..(6163)

20   <220>
    <221> CDS
    <222> (283)..(2793)

    <400> 3
25   ccaacgccgc aatggggagt agtagggacc cagcaacccg gtgccgggag ccctgcaccc
    60

    tgggagggag aggcggtcgc tgaggcagga agaggaggag gagagagagg agggacgcac
    120

30   cggggtcagct cgcgatcctg ctgcgcaggg cggggctcgg gccggtccgc ccgcgcgcag
    180

    gtgagtgagc cagggcggag cgcagctgcg ccgggcttgg gcgcctgggg ccgccgctcc
    240

35   ccaccgtcgt tttccccacc gaggccgagg cgtcccggag tc atg gcc ggc ctg
    294

                                     Met Ala Gly Leu
                                     1

40   aac tgc ggg gtc tct atc gca ctg cta ggg gtt ctg ctg ctg ggt gcg
    342
    Asn Cys Gly Val Ser Ile Ala Leu Leu Gly Val Leu Leu Leu Gly Ala
       5          10          15          20

45   gcg cgc ctg ccg cgc ggg gca gaa gct ttt gag att gct ctg cca cga
    390
    Ala Arg Leu Pro Arg Gly Ala Glu Ala Phe Glu Ile Ala Leu Pro Arg
          25          30          35

50   gaa agc aac att aca gtt ctc ata aag ctg ggg acc ccg act ctg ctg
    438
    Glu Ser Asn Ile Thr Val Leu Ile Lys Leu Gly Thr Pro Thr Leu Leu
          40          45          50

55   gca aaa ccc tgt tac atc gtc att tct aaa aga cat ata acc atg ttg
    486
    Ala Lys Pro Cys Tyr Ile Val Ile Ser Lys Arg His Ile Thr Met Leu

```

	55	60	65
	tcc atc aag tct gga gaa aga ata gtc ttt acc ttt agc tgc cag agt		
5	Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser		
	70	75	80
	cct gag aat cac ttt gtc ata gag atc cag aaa aat att gac tgt atg		
10	Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met		
	85	90	95
	tca ggc cca tgt cct ttt ggg gag gtt cag ctt cag ccc tcg aca tcg		
15	Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser		
	105	110	115
	ttg ttg cct acc ctc aac aga act ttc atc tgg gat gtc aaa gct cat		
20	Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp Val Lys Ala His		
	120	125	130
	aag agc atc ggt tta gag ctg cag ttt tcc atc cct cgc ctg agg cag		
25	Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln		
	135	140	145
	atc ggt ccg ggt gag agc tgc cca gac gga gtc act cac tcc atc agc		
30	Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser		
	150	155	160
	ggc cga atc gat gcc acc gtg gtc agg atc gga acc ttc tgc agc aat		
35	Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn		
	165	170	175
	ggc act gtg tcc cgg atc aag atg caa gaa gga gtg aaa atg gcc tta		
40	Gly Thr Val Ser Arg Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu		
	185	190	195
	cac ctc cca tgg ttc cac ccc aga aat gtc tcc ggc ttc agc att gca		
45	His Leu Pro Trp Phe His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala		
	200	205	210
	aac cgc tca tct ata aaa cgt ctg tgc atc atc gag tct gtg ttt gag		
50	Asn Arg Ser Ser Ile Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu		
	215	220	225
	ggt gaa ggc tca gca acc ctg atg tct gcc aac tac cca gaa ggc ttc		
55	Gly Glu Gly Ser Ala Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe		
	230	235	240

cct gag gat gag ctc atg acg tgg cag ttt gtc gtt cct gca cac ctg
 1062
 Pro Glu Asp Glu Leu Met Thr Trp Gln Phe Val Val Pro Ala His Leu
 245 250 255 260
 5 cgg gcc agc gtc tcc ttc ctc aac ttc aac ctc tcc aac tgt gag agg
 1110
 Arg Ala Ser Val Ser Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg
 265 270 275
 10 aag gag gag cgg gtt gaa tac tac atc ccg ggc tcc acc acc aac ccc
 1158
 Lys Glu Glu Arg Val Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro
 280 285 290
 15 gag gtg ttc aag ctg gag gac aag cag cct ggg aac atg gcg ggg aac
 1206
 Glu Val Phe Lys Leu Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn
 295 300 305
 20 ttc aac ctc tct ctg caa ggc tgt gac caa gat gcc caa agt cca ggg
 1254
 Phe Asn Leu Ser Leu Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly
 310 315 320
 25 atc ctc cgg ctg cag ttc caa gtt ttg gtc caa cat cca caa aat gaa
 1302
 Ile Leu Arg Leu Gln Phe Gln Val Leu Val Gln His Pro Gln Asn Glu
 325 330 335 340
 30 agc aat aaa atc tac gtg gtt gac ttg agt aat gag cga gcc atg tca
 1350
 Ser Asn Lys Ile Tyr Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser
 345 350 355
 35 ctc acc atc gag cca cgg ccc gtc aaa cag agc cgc aag ttt gtc cct
 1398
 40 Leu Thr Ile Glu Pro Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro
 360 365 370
 ggc tgt ttc gtg tgt cta gaa tct cgg acc tgc agt agc aac ctc acc
 1446
 45 Gly Cys Phe Val Cys Leu Glu Ser Arg Thr Cys Ser Ser Asn Leu Thr
 375 380 385
 ctg aca tct ggc tcc aaa cac aaa atc tcc ttc ctt tgt gat gat ctg
 1494
 50 Leu Thr Ser Gly Ser Lys His Lys Ile Ser Phe Leu Cys Asp Asp Leu
 390 395 400
 aca cgt ctg tgg atg aat gtg gaa aaa acc ata agc tgc aca gac cac
 1542
 55 Thr Arg Leu Trp Met Asn Val Glu Lys Thr Ile Ser Cys Thr Asp His
 405 410 415 420

cgg tac tgc caa agg aaa tcc tac tca ctc cag gtg ccc agt gac atc
 1590
 Arg Tyr Cys Gln Arg Lys Ser Tyr Ser Leu Gln Val Pro Ser Asp Ile
 425 430 435
 5 ctc cac ctg cct gtg gag ctg cat gac ttc tcc tgg aag ctg ctg gtg
 1638
 Leu His Leu Pro Val Glu Leu His Asp Phe Ser Trp Lys Leu Leu Val
 440 445 450
 10 ccc aag gac agg ctc agc ctg gtg ctg gtg cca gcc cag aag ctg cag
 1686
 Pro Lys Asp Arg Leu Ser Leu Val Leu Val Pro Ala Gln Lys Leu Gln
 455 460 465
 15 cag cat aca cac gag aag ccc tgc aac acc agc ttc agc tac ctc gtg
 1734
 Gln His Thr His Glu Lys Pro Cys Asn Thr Ser Phe Ser Tyr Leu Val
 470 475 480
 20 gcc agt gcc ata ccc agc cag gac ctg tac ttc ggc tcc ttc tgc ccg
 1782
 Ala Ser Ala Ile Pro Ser Gln Asp Leu Tyr Phe Gly Ser Phe Cys Pro
 485 490 495 500
 25 gga ggc tct atc aag cag atc cag gtg aag cag aac atc tcg gtg acc
 1830
 Gly Gly Ser Ile Lys Gln Ile Gln Val Lys Gln Asn Ile Ser Val Thr
 505 510 515
 30 ctt cgc acc ttt gcc ccc agc ttc caa caa gag gcc tcc agg cag ggt
 1878
 Leu Arg Thr Phe Ala Pro Ser Phe Gln Gln Glu Ala Ser Arg Gln Gly
 520 525 530
 35 ctg acg gtg tcc ttt ata cct tat ttc aaa gag gaa ggc gtt ttc acg
 1926
 Leu Thr Val Ser Phe Ile Pro Tyr Phe Lys Glu Glu Gly Val Phe Thr
 535 540 545
 40 gtg acc cct gac aca aaa agc aag gtc tac ctg agg acc ccc aac tgg
 1974
 Val Thr Pro Asp Thr Lys Ser Lys Val Tyr Leu Arg Thr Pro Asn Trp
 550 555 560
 45 gac cgg ggc ctg cca tcc ctc acc tct gtg tcc tgg aac atc agc gtg
 2022
 Asp Arg Gly Leu Pro Ser Leu Thr Ser Val Ser Trp Asn Ile Ser Val
 565 570 575 580
 50 ccc aga gac cag gtg gcc tgc ctg act ttc ttt aag gag cgg agc ggc
 2070
 55 Pro Arg Asp Gln Val Ala Cys Leu Thr Phe Phe Lys Glu Arg Ser Gly
 585 590 595

gtg gtc tgc cag aca ggg cgc gca ttc atg atc atc cag gag cag cgg
 2118
 Val Val Cys Gln Thr Gly Arg Ala Phe Met Ile Ile Gln Glu Gln Arg
 600 605 610

5

acc cgg gct gag gag atc ttc agc ctg gac gag gat gtg ctc ccc aag
 2166
 Thr Arg Ala Glu Glu Ile Phe Ser Leu Asp Glu Asp Val Leu Pro Lys
 615 620 625

10

cca agc ttc cac cat cac agc ttc tgg gtc aac atc tct aac tgc agc
 2214
 Pro Ser Phe His His His Ser Phe Trp Val Asn Ile Ser Asn Cys Ser
 630 635 640

15

ccc acg agc ggc aag cag cta gac ctg ctc ttc tcg gtg aca ctt acc
 2262
 Pro Thr Ser Gly Lys Gln Leu Asp Leu Leu Phe Ser Val Thr Leu Thr
 645 650 655 660

20

cca agg act gtg gac ttg act gtc atc ctc atc gca gcg gtg gga ggt
 2310
 Pro Arg Thr Val Asp Leu Thr Val Ile Leu Ile Ala Ala Val Gly Gly
 665 670 675

25

gga gtc tta ctg ctg tct gcc ctc ggg ctc atc att tgc tgt gtg aaa
 2358
 Gly Val Leu Leu Leu Ser Ala Leu Gly Leu Ile Ile Cys Cys Val Lys
 680 685 690

30

aag aag aaa aag aag aca aac aag ggc ccc gct gtg ggt atc tac aat
 2406
 Lys Lys Lys Lys Lys Thr Asn Lys Gly Pro Ala Val Gly Ile Tyr Asn
 695 700 705

35

ggc aac atc aat act gag atg ccg agg cag cca aaa aag ttt cag aaa
 2454
 Gly Asn Ile Asn Thr Glu Met Pro Arg Gln Pro Lys Lys Phe Gln Lys
 710 715 720

40

ggg cga aag gac aat gac tcc cat gtg tat gca gtc atc gag gac acc
 2502
 Gly Arg Lys Asp Asn Asp Ser His Val Tyr Ala Val Ile Glu Asp Thr
 725 730 735 740

45

atg gta tat ggg cat ctg cta cag gat tcc agc ggc tcc ttc ctg cag
 2550
 Met Val Tyr Gly His Leu Leu Gln Asp Ser Ser Gly Ser Phe Leu Gln
 745 750 755

50

cca gag gtg gac acc tac cgg ccg ttc cag ggc acc atg ggg gtc tgt
 2598
 Pro Glu Val Asp Thr Tyr Arg Pro Phe Gln Gly Thr Met Gly Val Cys
 760 765 770

55

cct ccc tcc cca ccc acc ata tgc tcc agg gcc cca act gca aag ttg
 2646
 Pro Pro Ser Pro Pro Thr Ile Cys Ser Arg Ala Pro Thr Ala Lys Leu

	775	780	785
	gcc act gag gag cca cct cct cgc tcc cct cct gag tct gag agt gaa 2694		
5	Ala Thr Glu Glu Pro Pro Pro Arg Ser Pro Pro Glu Ser Glu Ser Glu 790 795 800		
10	ccg tac acc ttc tcc cat ccc aac aat ggg gat gta agc agc aag gac 2742 Pro Tyr Thr Phe Ser His Pro Asn Asn Gly Asp Val Ser Ser Lys Asp 805 810 815 820		
15	aca gac att ccc tta ctg aac act cag gag ccc atg gag cca gca gaa 2790 Thr Asp Ile Pro Leu Leu Asn Thr Gln Glu Pro Met Glu Pro Ala Glu 825 830 835		
20	taa ctgatccat tccagacgct ttgctgagtt tcataaagca gggcactgag 2843		
25	acacccgtcc gtgttcctaa ccagaaatcc taaagaagag gaattataca gaaggaacag 2903 caggaggttt tcctggacac cgccaacttc acattgctca gtggactcat tctaagggca 2963		
30	agacattgaa aatgatgaat tccaatctgg atacagtcat gacagctcat gtgctcctca 3023		
35	acttaggctg tgcggttagc cagcctgtaa tgagaggaga gaggcctgag tcacctagca 3083 tagggttgca gcaagccctg gattcagagt gttaaacaga ggcttgcct cttcaggaca 3143		
40	acagttccaa ttccaaggag cctacctgag gtccctactc tcaactggggt ccccaggatg 3203		
45	aaaacgacaa tgtgcctttt tattattatt tatttgggtgg tcctgtgtta ttttaagagat 3263		
50	caaattgtata accacctagc tcttttcacc tgacttagta ataactcata ctaactgggt 3323 tggtgacctg ggttgtgact tctactgacc gctagataaa cgtgtgcctg tccccagggt 3383		
55	ggtgggaata atttacaatc tgtccaacca gaaaagaatg tgtgtgtttg agcagcattg 3443 acacatatct gctttgataa gagacttcct gattctctag gtcgggttcgt gggtatccca 3503 ttgtggaaat tcattcttgaa tcccattgtc ctatagtcct agcaataaga gaaatttcct 3563		

caagtttcca tgtgcggttc tcctagctgc agcaatactt tgacatttaa agagaaattt
 3623

5 agagaatatt ctcatcctct aaaaatgttt aaatatatac caaacagtgg cccctgcat
 3683

tagttttctg ttgccactgc aaccattac ttggtagctt aaaaacaaca cattagctta
 3743

10 tagtcctggg gatcagaatt ccaaaatgga tgtccctgaa tgaaaatcaa ggtgtcagca
 3803

15 gagctgtgct ccttctgaag gctctaggga gaagccggtt ccttgccatt tcaagcttct
 3863

agaggctggc tgcattccca ggctccagtg gctggtaag cttttctcac atggcatcac
 3923

20 tgtgacactg gccctccac ttccctcttt gacttacaaa gccaccagg aagatccagg
 3983

ataatctctc catctaaaga tccttcatca tcttgaaga gccttttgcc atgcaagaca
 4043

25 acatagccac aggtggggat taggaccagg acatctttgg ggtgctgtta ttctgcctac
 4103

30 cacaccttcc tgccactgac tcccacagga gaggtacaa aatgatctgg cgcacagggg
 4163

tgttttgttt agcttgcgga ctctaact taaaaaacc ccagatcaga agatctggcc
 4223

35 atgctggggc tcacattctc acctagcaac aactggctgg agctgggcac cagctctgcc
 4283

tttagaaggg gtgtccactt caccaggta ccacagccca cactacgcc tatcacttcc
 4343

40 cacaatgagg ctaagtgttt gtttctactg atcaatgccc ctgcagggtg catttattgt
 4403

45 aatgaaaaag aaagactggg attaattctc aatcagggtg gtagaccatg agaccaatgt
 4463

gtgctcacat tacccttttt cttttttttt tttttctttt tctttttttt tttaatgtga
 4523

50 gacaggatct cattctgttg cctaggctgg agtgacagtgg cgcaatctcg gctcactgca
 4583

acctctgcct cctgggctca agcaattctc ccacctcagc ctcccaaata gctgggatca
 4643

55 ctggcacaaa ccaccatgcc cagctaattt tgtatttttt gtagagacag ggtttcacca
 4703

tgttgcccag gctggtctca acctcctggg ctcaagcaat cctcctgcct cggcctccca
 4763
 5 aagtgctggg attacagatg tgagccaccg catccagccc cacaccctca tttataccaa
 4823
 ttacctgccc agtaactgtg gacttttgct tctcaccccc tgctctgatc tggaaggaga
 4883
 10 gggattatgt tatagcttgt cagcacagtc ccaagttcaa tatttctgcg gcaaaaactt
 4943
 ccttcaaaaa ataaatgtac ttcattgtat tcaatgaatt caccttgga atgcaccgcc
 5003
 15 tcaacttggt cacatggcat aaatgaaagg aattttatag tctcctaaat ggcgtgtact
 5063
 gcaagacctc ttgaacactt tccagaggat aggatattta agtcatgccc ttggcgttgc
 20 5123
 ctatggcacc tttcccttct gaaagtctgg ttctgcccc gtgacccttg gccttgtgag
 5183
 25 ccgagatgct gaccctgcat aaagggccaa aggagggctg cggcttcctt ccctcactga
 5243
 agagccctta tttgaattca ctgtgtggag ccctagccct ccattctcga cattccccaa
 5303
 30 cctccagacc ccttccaagc aggactaggt gccctgcatt ccaccaagg tgggattggc
 5363
 cttccttagg ctggctactt gtcaccatca ccgacatcac tgttgccctgc aaggacacca
 35 5423
 cgtggccatt ttccttcaac tgagggctca aaactcctgg acaagttgct ggctcctgag
 5483
 40 accagtattt cctggagctg tgccctcagt aaggggcccc gcctgaggaa ccctggctct
 5543
 tttctttaaa gcccaggccc cacttacata aaacatttca gggtcactgg aaacagtga
 5603
 45 gtgccatttg ttgaagccta ctgcatgcca gccactgct catccacgtg gtctgccatg
 5663
 cctacgagga aggccagcgc atgcaggact ggtctctaat gctgtggtca ttgcacagaa
 50 5723
 gggaaaggct tcaaggaaga gtcaactggg acaagcacia gccaccgga catggccttg
 5783
 55 gtaaagggtta gcagactggt gtgtgtggat ctgcagtgct tcaactgaaa taatttatc
 5843

```

attgcagata ctttttaggt ggcattttat tcatttcctg tgctttaaat aaacaaatgt
5903

accaaaaaaac aagtatcaag ctgtttaagt gcttcggcta cttgtcccct gggtcagtag
5 5963

aggccccggt ttcccagttg ttgactgtga caggctcagc atgggctcag cagatgctgt
6023

10 ctttaattgt ggatgataca gaaagccagg ctttgggata caagttcttt cctcttcatt
6083

tgatgccgtg cactgtgtga agcagatggt tttgtccgga aataaaaaata atagtcttgg
6143
15 agtctcgcca aaaaaaaaaa
6163

20
<210> 4
<211> 836
<212> PRT
<213> Homo sapiens
25
<400> 4
Met Ala Gly Leu Asn Cys Gly Val Ser Ile Ala Leu Leu Gly Val Leu
1 5 10 15
30 Leu Leu Gly Ala Ala Arg Leu Pro Arg Gly Ala Glu Ala Phe Glu Ile
20 25 30
Ala Leu Pro Arg Glu Ser Asn Ile Thr Val Leu Ile Lys Leu Gly Thr
35 35 40 45
35 Pro Thr Leu Leu Ala Lys Pro Cys Tyr Ile Val Ile Ser Lys Arg His
50 55 60
40 Ile Thr Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe
65 70 75 80
Ser Cys Gln Ser Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn
85 90 95
45 Ile Asp Cys Met Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln
100 105 110
Pro Ser Thr Ser Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp
115 120 125
50 Val Lys Ala His Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro
130 135 140
55 Arg Leu Arg Gln Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr
145 150 155 160
His Ser Ile Ser Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr
165 170 175

```

	Phe	Cys	Ser	Asn	Gly	Thr	Val	Ser	Arg	Ile	Lys	Met	Gln	Glu	Gly	Val	
				180					185					190			
5	Lys	Met	Ala	Leu	His	Leu	Pro	Trp	Phe	His	Pro	Arg	Asn	Val	Ser	Gly	
			195					200					205				
	Phe	Ser	Ile	Ala	Asn	Arg	Ser	Ser	Ile	Lys	Arg	Leu	Cys	Ile	Ile	Glu	
		210					215					220					
10																	
	Ser	Val	Phe	Glu	Gly	Glu	Gly	Ser	Ala	Thr	Leu	Met	Ser	Ala	Asn	Tyr	
	225					230					235					240	
15	Pro	Glu	Gly	Phe	Pro	Glu	Asp	Glu	Leu	Met	Thr	Trp	Gln	Phe	Val	Val	
					245					250					255		
	Pro	Ala	His	Leu	Arg	Ala	Ser	Val	Ser	Phe	Leu	Asn	Phe	Asn	Leu	Ser	
				260					265					270			
20																	
	Asn	Cys	Glu	Arg	Lys	Glu	Glu	Arg	Val	Glu	Tyr	Tyr	Ile	Pro	Gly	Ser	
			275					280					285				
	Thr	Thr	Asn	Pro	Glu	Val	Phe	Lys	Leu	Glu	Asp	Lys	Gln	Pro	Gly	Asn	
25		290					295					300					
	Met	Ala	Gly	Asn	Phe	Asn	Leu	Ser	Leu	Gln	Gly	Cys	Asp	Gln	Asp	Ala	
	305					310					315					320	
30																	
	Gln	Ser	Pro	Gly	Ile	Leu	Arg	Leu	Gln	Phe	Gln	Val	Leu	Val	Gln	His	
					325					330					335		
	Pro	Gln	Asn	Glu	Ser	Asn	Lys	Ile	Tyr	Val	Val	Asp	Leu	Ser	Asn	Glu	
				340					345					350			
35																	
	Arg	Ala	Met	Ser	Leu	Thr	Ile	Glu	Pro	Arg	Pro	Val	Lys	Gln	Ser	Arg	
			355					360					365				
	Lys	Phe	Val	Pro	Gly	Cys	Phe	Val	Cys	Leu	Glu	Ser	Arg	Thr	Cys	Ser	
40		370					375					380					
	Ser	Asn	Leu	Thr	Leu	Thr	Ser	Gly	Ser	Lys	His	Lys	Ile	Ser	Phe	Leu	
	385					390					395					400	
45																	
	Cys	Asp	Asp	Leu	Thr	Arg	Leu	Trp	Met	Asn	Val	Glu	Lys	Thr	Ile	Ser	
					405					410					415		
	Cys	Thr	Asp	His	Arg	Tyr	Cys	Gln	Arg	Lys	Ser	Tyr	Ser	Leu	Gln	Val	
				420					425					430			
50																	
	Pro	Ser	Asp	Ile	Leu	His	Leu	Pro	Val	Glu	Leu	His	Asp	Phe	Ser	Trp	
			435					440					445				
	Lys	Leu	Leu	Val	Pro	Lys	Asp	Arg	Leu	Ser	Leu	Val	Leu	Val	Pro	Ala	
55		450					455					460					
	Gln	Lys	Leu	Gln	Gln	His	Thr	His	Glu	Lys	Pro	Cys	Asn	Thr	Ser	Phe	
	465					470					475					480	

	Ser	Tyr	Leu	Val	Ala	Ser	Ala	Ile	Pro	Ser	Gln	Asp	Leu	Tyr	Phe	Gly	
					485					490					495		
5	Ser	Phe	Cys	Pro	Gly	Gly	Ser	Ile	Lys	Gln	Ile	Gln	Val	Lys	Gln	Asn	
				500					505					510			
	Ile	Ser	Val	Thr	Leu	Arg	Thr	Phe	Ala	Pro	Ser	Phe	Gln	Gln	Glu	Ala	
			515					520					525				
10																	
	Ser	Arg	Gln	Gly	Leu	Thr	Val	Ser	Phe	Ile	Pro	Tyr	Phe	Lys	Glu	Glu	
		530					535					540					
15	Gly	Val	Phe	Thr	Val	Thr	Pro	Asp	Thr	Lys	Ser	Lys	Val	Tyr	Leu	Arg	
	545					550					555					560	
	Thr	Pro	Asn	Trp	Asp	Arg	Gly	Leu	Pro	Ser	Leu	Thr	Ser	Val	Ser	Trp	
				565						570					575		
20																	
	Asn	Ile	Ser	Val	Pro	Arg	Asp	Gln	Val	Ala	Cys	Leu	Thr	Phe	Phe	Lys	
				580					585					590			
	Glu	Arg	Ser	Gly	Val	Val	Cys	Gln	Thr	Gly	Arg	Ala	Phe	Met	Ile	Ile	
25			595					600					605				
	Gln	Glu	Gln	Arg	Thr	Arg	Ala	Glu	Glu	Ile	Phe	Ser	Leu	Asp	Glu	Asp	
		610					615					620					
30	Val	Leu	Pro	Lys	Pro	Ser	Phe	His	His	His	Ser	Phe	Trp	Val	Asn	Ile	
	625					630					635					640	
	Ser	Asn	Cys	Ser	Pro	Thr	Ser	Gly	Lys	Gln	Leu	Asp	Leu	Leu	Phe	Ser	
				645						650					655		
35																	
	Val	Thr	Leu	Thr	Pro	Arg	Thr	Val	Asp	Leu	Thr	Val	Ile	Leu	Ile	Ala	
				660					665					670			
	Ala	Val	Gly	Gly	Gly	Val	Leu	Leu	Leu	Ser	Ala	Leu	Gly	Leu	Ile	Ile	
40			675					680					685				
	Cys	Cys	Val	Lys	Lys	Lys	Lys	Lys	Lys	Thr	Asn	Lys	Gly	Pro	Ala	Val	
		690					695					700					
45	Gly	Ile	Tyr	Asn	Gly	Asn	Ile	Asn	Thr	Glu	Met	Pro	Arg	Gln	Pro	Lys	
	705					710					715					720	
	Lys	Phe	Gln	Lys	Gly	Arg	Lys	Asp	Asn	Asp	Ser	His	Val	Tyr	Ala	Val	
				725						730					735		
50																	
	Ile	Glu	Asp	Thr	Met	Val	Tyr	Gly	His	Leu	Leu	Gln	Asp	Ser	Ser	Gly	
				740					745					750			
	Ser	Phe	Leu	Gln	Pro	Glu	Val	Asp	Thr	Tyr	Arg	Pro	Phe	Gln	Gly	Thr	
55			755					760					765				
	Met	Gly	Val	Cys	Pro	Pro	Ser	Pro	Pro	Thr	Ile	Cys	Ser	Arg	Ala	Pro	
		770					775					780					

Thr Ala Lys Leu Ala Thr Glu Glu Pro Pro Pro Arg Ser Pro Pro Glu
 785 790 795 800

5 Ser Glu Ser Glu Pro Tyr Thr Phe Ser His Pro Asn Asn Gly Asp Val
 805 810 815

Ser Ser Lys Asp Thr Asp Ile Pro Leu Leu Asn Thr Gln Glu Pro Met
 820 825 830

10 Glu Pro Ala Glu
 835

15

<210> 5
 <211> 23
 <212> DNA

20 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: Primer

25 <400> 5
 accgcctcaa cttgttcaca tgg
 23

30

<210> 6
 <211> 26
 <212> DNA
 <213> Artificial sequence

35

<220>
 <223> Description of the artificial sequence: Primer

<400> 6

40 ctggtctcag gagccagcaa cttgtc
 26

45

<210> 7
 <211> 25
 <212> DNA
 <213> Artificial sequence

50

<220>
 <223> Description of the artificial sequence: Primer

<400> 7

55 ctcatgacgt ggcagtttgt cgttc
 25

<210> 8
<211> 26
<212> DNA
<213> Artificial sequence
5
<220>
<223> Description of the artificial sequence: Primer

<400> 8
10 ggctcgctca ttactcaagt caacca
26

15
<210> 9
<211> 36
<212> DNA
<213> Artificial sequence
20
<220>
<223> Description of the artificial sequence: Primer

<400> 9
25 attcgcgact gatgatcgat tttttttttt tttttt
36

30 <210> 10
<211> 20
<212> DNA
<213> Artificial sequence
35 <220>
<223> Description of the artificial sequence: Primer

<400> 10
40 attcgcgact gatgatcgat
20

45 <210> 11
<211> 20
<212> DNA
<213> Artificial sequence

<220>
50 <223> Description of the artificial sequence: Primer

<400> 11
gagatattag aattctactc
20
55

<210> 12

<211> 17
<212> DNA
<213> Artificial sequence

5 <220>
<223> Description of the artificial sequence: Primer

<400> 12
gagtagaatt ctaatat
10 17

15 <210> 13
<211> 22
<212> DNA
<213> Artificial sequence

20 <220>
<223> Description of the artificial sequence: Primer

<400> 13
agtccatgtg aacaagttga gg
22
25

30 <210> 14
<211> 20
<212> DNA
<213> Artificial sequence

35 <220>
<223> Description of the artificial sequence: Primer

<400> 14
aattctccca cctcagcctc
20
40

45 <210> 15
<211> 22
<212> DNA
<213> Artificial sequence

50 <220>
<223> Description of the artificial sequence: Primer

<400> 15
aggatgaaaa cgacaatgtg cc
22

55 <210> 16
<211> 21
<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

5 <400> 16
agaattgctt gagcccagga g
21

10

<210> 17
<211> 21
<212> DNA

15 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

20 <400> 17
caacttcaca ttgctcagt g
21

25 <210> 18
<211> 25
<212> DNA

<213> Artificial sequence

30 <220>

<223> Description of the artificial sequence: Primer

<400> 18
tgagcaagtt cagcctgggt aagtc

35 25

40 <210> 19
<211> 26
<212> DNA

<213> Artificial sequence

<220>

45 <223> Description of the artificial sequence: Primer

<400> 19
caccgaatac tcataaagaa ggtccc

50 26

<210> 20
<211> 26
<212> DNA

55 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer
<400> 20
tagacttcga gcaggagatg gccact
5 26

<210> 21
10 <211> 20
<212> DNA
<213> Artificial sequence

<220>
15 <223> Description of the artificial sequence: Primer
<400> 21
ccagccatgt acgtagccat
20 20

<210> 22
<211> 19
25 <212> DNA
<213> Artificial sequence

<220>
30 <223> Description of the artificial sequence: Primer
<400> 22
ccaagaagga aggctggaa
19

35
<210> 23
<211> 25
<212> DNA
40 <213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
45 <400> 23
ccatcaccat cttccaggag cgaga
25

50
<210> 24
<211> 19
<212> DNA
<213> Artificial sequence
55
<220>
<223> Description of the artificial sequence: Primer

<400> 24
ccaagaagga aggctggaa
19

5

<210> 25
<211> 20
<212> DNA

10 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

15

<400> 25
tgcaggaggc attgctgatg
20

20

<210> 26
<211> 19
<212> DNA

<213> Artificial sequence

25

<220>

<223> Description of the artificial sequence: Primer

30

<400> 26
aaatcgtgca cttgcaggc
19

35

<210> 27
<211> 18
<212> DNA

<213> Artificial sequence

<220>

40 <223> Description of the artificial sequence: Primer

<400> 27
ttgatgcggt ccagctga
18

45

<210> 28
<211> 21
<212> DNA

50

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

55

<400> 28
ttgaattcac tgtgtggagc c
21

5 <210> 29
 <211> 19
 <212> DNA
 <213> Artificial sequence

10 <220>
 <223> Description of the artificial sequence: Primer

15 <400> 29
 tgcaggcaac agtgatgtc
 19

20 <210> 30
 <211> 24
 <212> DNA
 <213> Artificial sequence

25 <220>
 <223> Description of the artificial sequence: Primer

30 <400> 30
 attggccttc cttaggctgg ctac
 24

35 <210> 31
 <211> 43
 <212> DNA
 <213> Artificial sequence

40 <220>
 <223> Description of the artificial sequence: Primer

45 <400> 31
 tgtagcgtga agacgacaga aagggcgtgg taccgagctc gag
 43

50 <210> 32
 <211> 22
 <212> DNA
 <213> Artificial sequence

55 <220>
 <223> Description of the artificial sequence: Primer

 <400> 32
 agggcgtggt accgagctcg ag
 22

<210> 33
<211> 11
<212> DNA
5 <213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer

10 <400> 33
ggctcgagct c
11

15
<210> 34
<211> 22
<212> DNA
<213> Artificial sequence
20
<220>
<223> Description of the artificial sequence: Primer

<400> 34
25 ggccatgtcc ggtgggcttg tg
22

30 <210> 35
<211> 26
<212> DNA
<213> Artificial sequence
35 <220>
<223> Description of the artificial sequence: Primer

<400> 35
ctcaaaactc ctggacaagt tgctgg
40 26

<210> 36
<211> 22
45 <212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
50
<400> 36
aaggtgaagg tcggagtcaa cg
22

55

<210> 37
<211> 24

<212> DNA
<213> Artificial sequence

<220>
5 <223> Description of the artificial sequence: Primer

<400> 37
ggcagagatg atgacccttt tggc
24

10

<210> 38
<211> 23
15 <212> DNA
<213> Artificial sequence

<220>
<221> 5'UTR
20 <222> (1)..(282)

<220>
<221> GC_signal
<222> (147)..(157)

25

<220>
<221> misc_feature
<222> (201)..(209)
<223> cap signal; Transcription start

30

<220>
<221> 3'UTR
<222> (2794)..(6163)

35

<220>
<221> 3'UTR
<222> (2794)..(6163)

40

<220>
<221> CDS
<222> (283)..(2793)

<400> 38
agcagcagaa cccctagcag tgc
45 23

<210> 39
<211> 26
50 <212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer

55

<400> 39
agaacccta gcagtgcgat agagac
26

5 <210> 40
<211> 27
<212> DNA
<213> Artificial sequence

10 <220>
<223> Description of the artificial sequence: Primer

<400> 40
gaactgtaat gttgctttct cgtggca
27

15